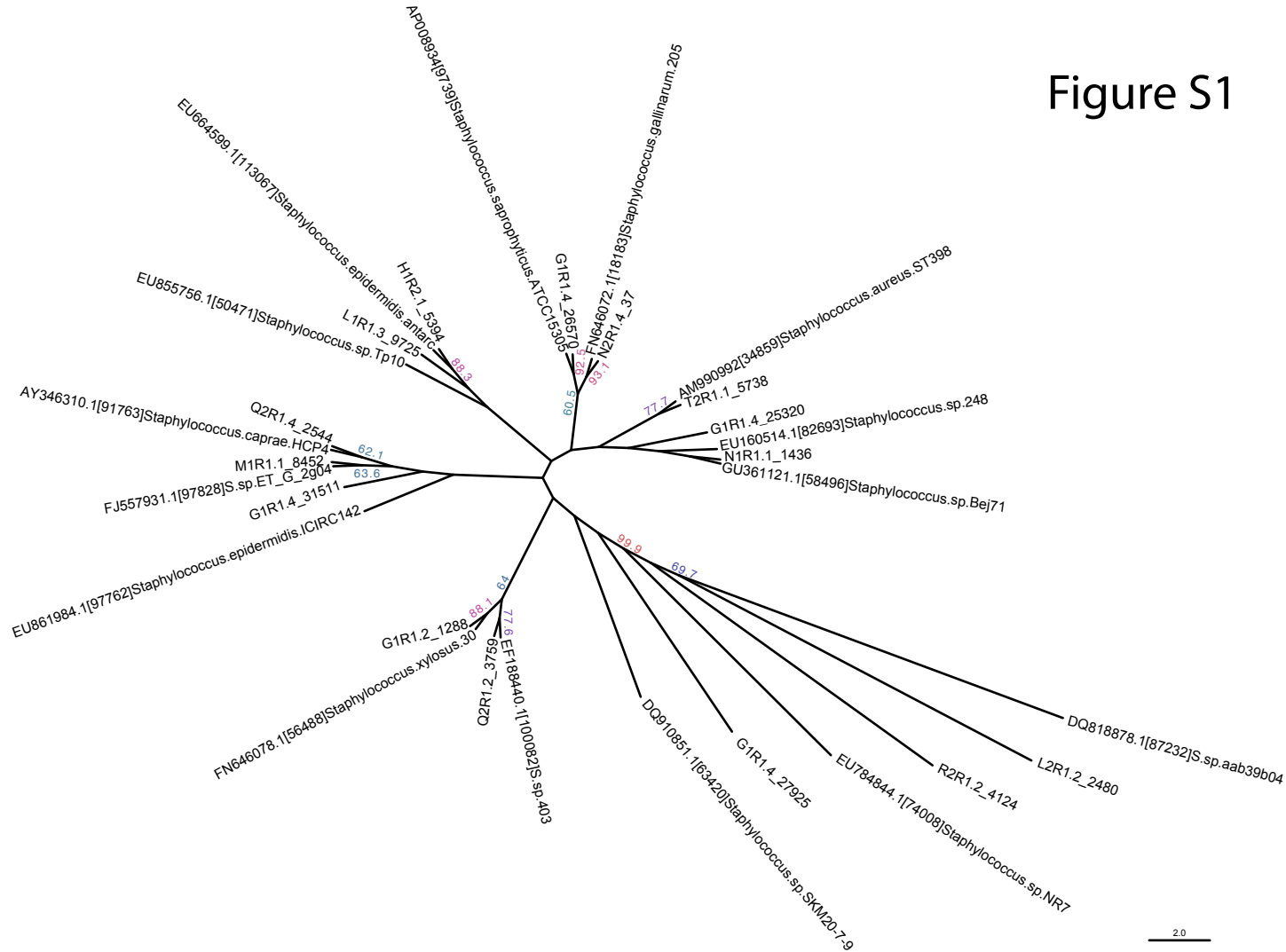


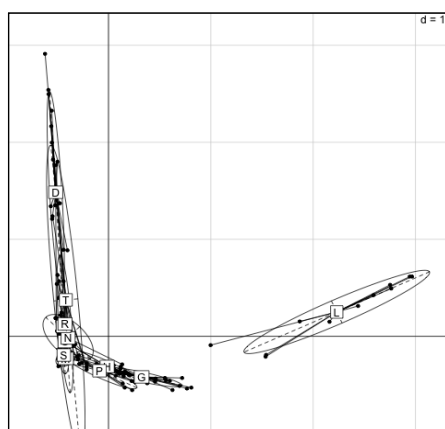
Supplemental Figures

A

Figure S1

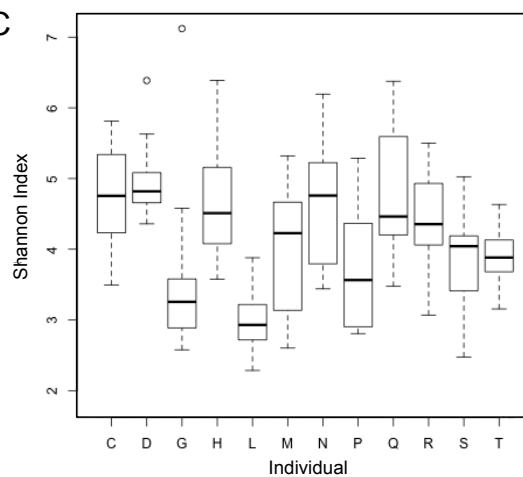


B

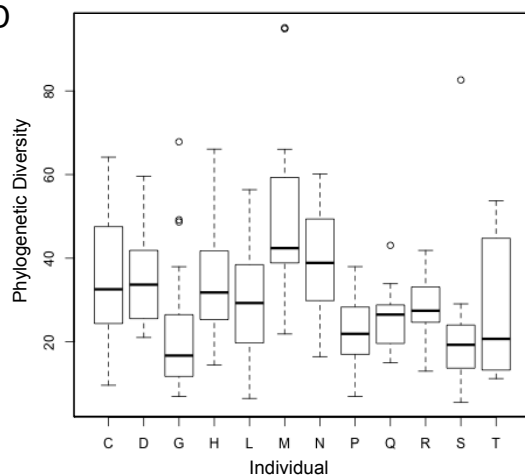


CoA scatterplot classified by individual

C



D



E

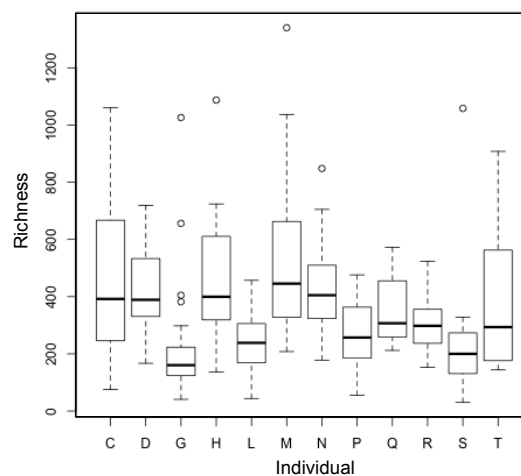


Figure S1. Phylogenetic analysis and diversity assessments of staphylococcal and other OTUs in subjects and individuals, related to Fig. 1. (A) Phylogenetic tree based on fifteen sequences representing the *Staphylococcus* OTUs found in the human nasal cavities together with the fifteen respective reference sequences from the SILVA 108 reference database. Sequences were aligned using SINA, alignments trimmed to the same length, and maximum likelihood inferred using PHYML. Bootstrap statistical support for branchings ≥ 60 are shown. Genbank accession numbers as well as the SILVA 108 reference database sequence number (in square brackets) are given. Percent sequence identity for the sequence pairs are as follows: T2R1.1_5738 to AM99099: 99.4%, Q2R1.4_2544 to AY346310: 99.4%, G1R1.4_31511 to EU861984.1: 99.4%, H1R2.1_5394 to EU664599.1: 99.4%, N2R1.4_37 to FN646072.1: 100%, G1R1.4_26570 to AP008934: 100%, G1R1.4_25320 to GU361121: 98.7%, R2R1.2_4124 to EU784844.1: 100%, G1R1.4_27925 to DQ910851.1: 100%, L1R1.3_9725 to EU855756.1: 99.4%, G1R1.2_1288 to FN646078.1: 98.7, L2R1.2_2480 to DQ818878.1: 100%, M1R1.1_8452 to FJ557931.1: 100%, Q2R1.2_3759 to EF188440.1: 100%, N1R1.1_1436 to EU160514.1: 99.4%. (B) Correspondence analysis and (C-E) alpha diversity calculations on abundance data show significant individual to individual variation, with individual “L” an apparent outlier. The bottom and top of each box are the first and third quartiles, respectively, and the band inside the box is the median. The whiskers represent one standard deviation above and below the mean of the data.

Figure S2

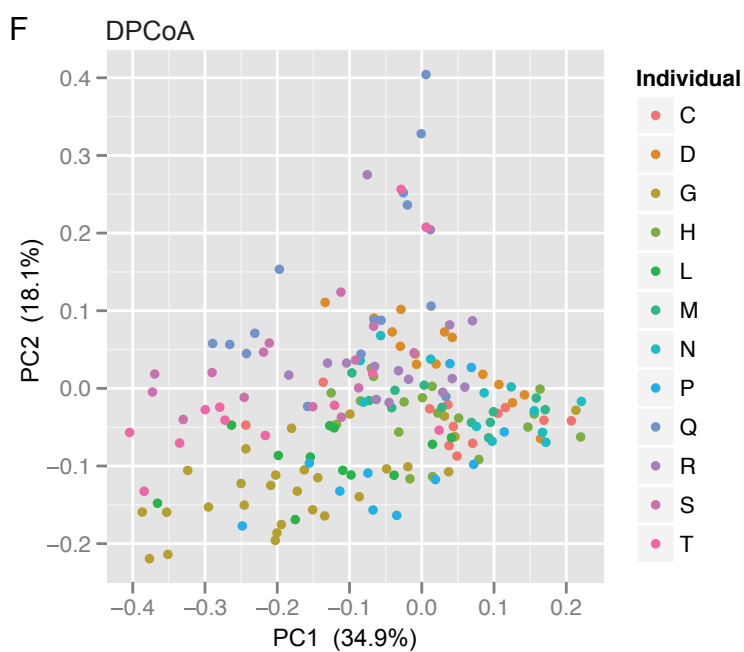
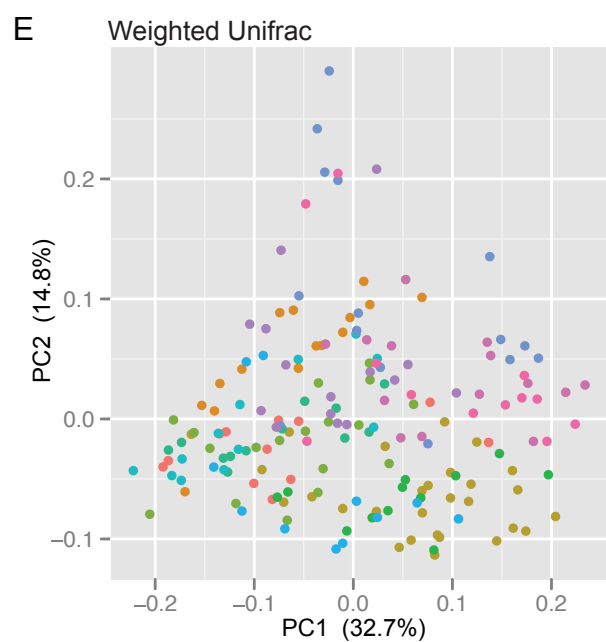
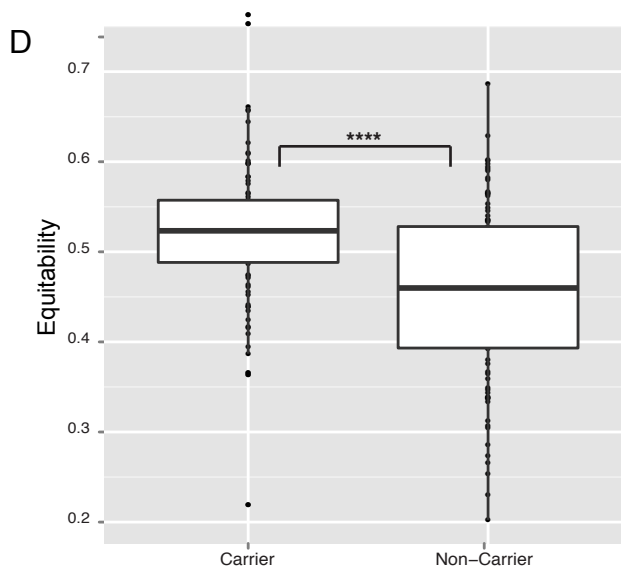
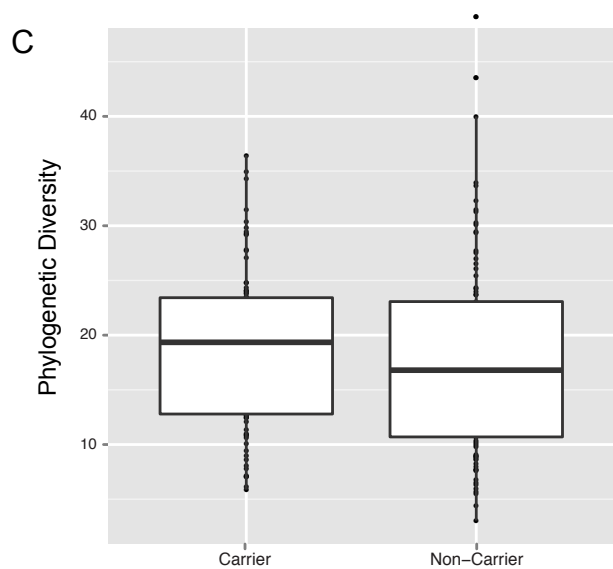
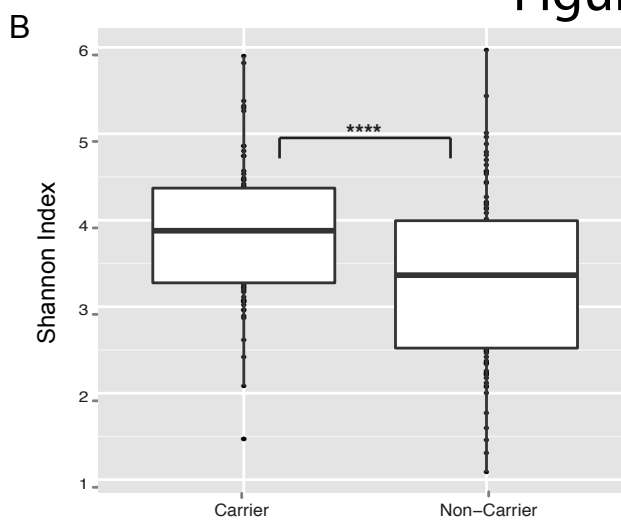
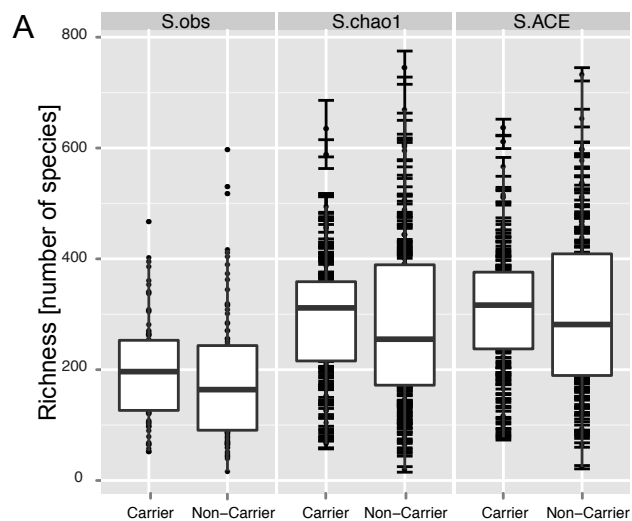


Figure S2. *Staphylococcus aureus* carriage type is associated with ecologically distinct communities, related to Fig. 2. Alpha diversity metrics in terms of (A) Richness, (B) Shannon diversity, (C) Phylogenetic diversity and (D) Equitability were compared for samples from *S. aureus* carriers versus non-carriers and tested for significance using the Wilcoxon Rank Sum test. The bottom and top of each box are the first and third quartiles, respectively, and the band inside the box is the median. Communities belonging to *S. aureus* carriers possessed a higher level of diversity ($P = 7.17 \times 10^{-6}$) and greater evenness ($P = 4.15 \times 10^{-5}$) than those of non-carriers. Species richness and phylogenetic diversity did not differ at a statistically significant level between carrier and non-carriers. Principal coordinate analysis of two separate phylogenetically-based distance metrics, namely (E) weighted UniFrac and (F) DPCoA, reveal an absence of strong clustering by individual.

Figure S3

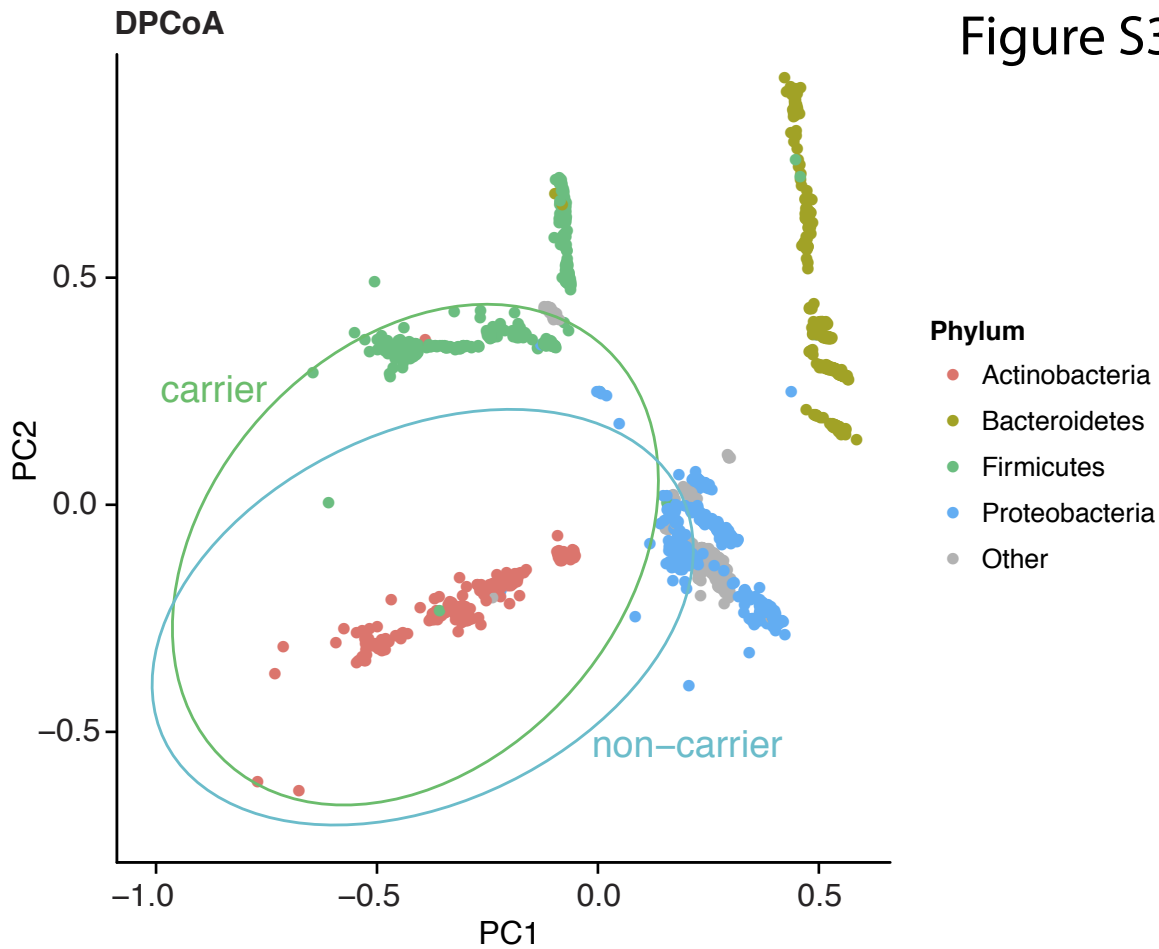


Figure S3. Phylum level differences are associated with separation of non-carrier communities from carrier communities, related to Fig. 4. DPCoA species plot with ellipses drawn around the weighted mean of the categories, *S. aureus* carrier and non-carrier.

Supplemental Tables

Table S1. Distance matrix displaying the percent sequence identities between the *Staphylococcus* OTUs found in the human nasal cavities compared with sequenced *Staphylococcus* type strains of the SILVA 111 LTP collection, related to Fig. 1. Dark blue indicates high sequence identity and light blue indicates low sequence identity. Sequence identities for the representative *Staphylococcus* sequence from the nasal cavity compared with their respective closest relative found in the SILVA type strain collection, are highlighted in white.

T2R1.1_5738																														
99.4	L36472 <i>Staphylococcus aureus</i>																													
96.2	96.8	Q2R1.4_2544																												
96.8	97.4	99.4	AB009935.1 <i>Staphylococcus caprae</i>																											
96.8	97.4	98.1	98.7	G1R1.4_31511																										
97.4	98.1	98.7	99.4	99.4	D83363.1 <i>Staphylococcus epidermidis</i>																									
96.2	96.8	96.2	96.8	96.8	97.4	H1R2.1_5394																								
96.2	96.8	96.2	96.8	96.8	97.4	100	AB009944.1 <i>Staphylococcus pasteurii</i>																							
97.4	98.1	94.9	95.5	95.5	96.2	94.9	94.9	N2R1.4_37																						
97.4	98.1	94.9	95.5	95.5	96.2	94.9	94.9	100	D83366.1 <i>Staphylococcus gallinarum</i>																					
95.5	96.2	95.5	96.2	96.2	96.8	96.8	96.8	98.1	98.1	G1R1.4_26570																				
95.5	96.2	95.5	96.2	96.2	96.8	96.8	96.8	98.1	98.1	100	AB233327.1 <i>Staphylococcus saprophyticus subsp. bovis</i>																			
98.1	98.7	96.8	97.4	97.4	98.1	98.1	98.1	96.8	96.8	97.4	97.4	G1R1.4_25320																		
97.4	98.1	97.4	98.1	98.1	98.7	97.4	97.4	96.2	96.2	96.8	96.8	99.4	X66100.1 <i>Staphylococcus haemolyticus</i>																	
93.6	94.2	93.6	94.2	94.2	94.9	93.6	93.6	92.3	92.3	92.9	92.9	94.2	93.6	R2R1.2_4124																
93.6	94.2	93.6	94.2	94.2	94.9	93.6	93.6	92.3	92.3	92.9	92.9	94.2	93.6	100	AJ421446.1 <i>Staphylococcus sciuri subsp. sciuri</i>															
98.1	98.7	98.1	98.7	98.7	99.4	98.1	98.1	96.8	96.8	97.4	97.4	98.7	98.1	95.5	95.5	G1R1.4_27925														
98.1	98.7	98.1	98.7	98.7	99.4	98.1	98.1	96.8	96.8	97.4	97.4	98.7	98.1	95.5	95.5	100	AB009936.1 <i>Staphylococcus cohnii</i>													
96.8	97.4	96.8	97.4	97.4	98.1	98.1	98.1	95.5	95.5	97.4	97.4	98.7	98.1	94.2	94.2	98.7	98.7	L1R1.3_9725												
96.8	97.4	96.8	97.4	97.4	98.1	98.1	98.1	95.5	95.5	97.4	97.4	98.7	98.1	94.2	94.2	98.7	98.7	98.7	AB009941.1 <i>Staphylococcus lugdunensis</i>											
96.8	97.4	95.5	96.2	96.2	96.8	95.5	95.5	96.8	96.8	96.2	96.2	96.2	95.5	92.9	92.9	97.4	97.4	96.2	96.2	G1R1.2_1288										
96.8	97.4	95.5	96.2	96.2	96.8	95.5	95.5	96.8	96.8	96.2	96.2	96.2	95.5	92.9	92.9	97.4	97.4	96.2	96.2	100	AF004220.1 <i>Staphylococcus succinus</i>									
92.9	93.6	92.9	93.6	93.6	94.2	92.9	92.9	91.7	91.7	92.3	92.3	93.6	92.9	99.4	99.4	94.9	94.9	93.6	94.9	92.3	92.3	L2R1.2_2480								
92.9	93.6	92.9	93.6	93.6	94.2	92.9	92.9	91.7	91.7	92.3	92.3	93.6	92.9	99.4	99.4	94.9	94.9	93.6	94.9	92.3	92.3	100	D83370.1 <i>Staphylococcus lentus</i>							
96.8	97.4	98.1	98.7	98.7	99.4	96.8	96.8	95.5	95.5	96.2	96.2	97.4	98.1	94.2	94.2	98.7	98.7	97.4	97.4	96.2	96.2	93.6	93.6	M1R1.1_8452						
96.8	97.4	98.1	98.7	98.7	99.4	96.8	96.8	95.5	95.5	96.2	96.2	97.4	98.1	94.2	94.2	98.7	98.7	97.4	97.4	96.2	96.2	93.6	93.6	98.7	L37602.1 <i>Staphylococcus saccharolyticus</i>					
96.8	97.4	96.8	97.4	97.4	98.1	96.8	96.8	95.5	95.5	96.2	96.2	97.4	96.8	94.2	94.2	98.7	98.7	97.4	97.4	98.7	98.7	93.6	93.6	97.4	97.4	Q2R1.2_3759				
96.8	97.4	96.8	97.4	97.4	98.1	96.8	96.8	95.5	95.5	96.2	96.2	97.4	96.8	94.2	94.2	98.7	98.7	97.4	97.4	98.7	98.7	93.6	93.6	97.4	97.4	100	D83358.1 <i>Staphylococcus auricularis</i>			
97.4	98.1	97.4	98.1	98.1	98.7	97.4	97.4	96.2	96.2	96.8	96.8	99.4	100	93.6	93.6	98.1	98.1	98.1	98.1	95.5	95.5	92.9	92.9	98.1	98.1	96.8	96.8	N1R1.1_1436		
97.4	98.1	97.4	98.1	98.1	98.7	97.4	97.4	96.2	96.2	96.8	96.8	99.4	100	93.6	93.6	98.1	98.1	98.1	98.1	95.5	95.5	92.9	92.9	98.1	98.1	96.8	96.8	100	FJ389206.1 <i>Staphylococcus devriesei</i>	

Table S2. OTUs that are significantly enriched in a particular tissue environment (Skin vs. Mucosa), based on ANOVA testing, related to Fig. 3. Relative OTU abundances for the skin-like environment (anterior naris) were compared with mucosa-like environments (middle meatus, sphenoethmoidal recess). P-values were corrected using the false discovery rate (FDR) method. Dark blue denotes enrichment in a particular tissue environment and light blue denotes significant lower abundance in the other tissue environment.

p-value (FDR corrected)	Skin	Mucosa	SILVA 108 OTU [ID]*
1.12E-2	1.29E-3	6.30E-3	[bP]g_Aquabacterium;s_Uncultured_bacterium_[96961]
1.20E-2	1.92E-3	6.84E-3	[bP]g_Alicyclophilus;s_Uncultured_bacterium_[95867]
1.43E-2	1.00E-3	3.13E-3	[gP]g_Escherichia-shigella;s_Uncultured_bacterium_[30527]
1.76E-2	2.20E-3	6.49E-3	[bP]g_Variovorax;s_Uncultured_bacterium_[94508]
1.90E-2	7.28E-4	3.08E-3	[bP]g_Delftia;s_Uncultured_bacterium_[80833]
1.92E-2	3.60E-4	1.35E-3	[bP]g_Ralstonia;s_Uncultured_bacterium_[56245]
1.99E-2	2.61E-4	4.95E-5	[F]g_Streptococcus;s_Uncultured_bacterium_[9786]
2.02E-2	2.10E-1	1.24E-1	[A]g_Propionibacterium;s_Propionibacterium_acnes_[92374]
2.05E-2	5.19E-2	1.29E-1	[gP]g_Escherichia-shigella;s_Uncultured_bacterium_[30769]
2.08E-2	1.82E-4	5.35E-5	[A]g_Actinokineospora;s_Actinokineospora_auranticolor_[87484]
2.23E-2	2.14E-4	9.90E-4	[gP]g_Pseudomonas;s_Pseudomonas_fluorescens_[6557]
2.25E-2	8.87E-5	3.68E-4	[bP]g_Uncultured;s_Uncultured_bacterium_[69569]
2.31E-2	5.02E-4	2.21E-3	[bP]g_Methyloversatilis;s_Uncultured_bacterium_[21666]
3.21E-2	4.69E-4	1.49E-3	[aP]g_Gobb3-c201;s_Uncultured_bacterium_[15257]
4.49E-2	8.20E-3	3.17E-3	[F]g_Staphylococcus;s_Staphylococcus_caprae_[91763]
4.49E-2	4.44E-4	2.00E-3	[C]g_Chloroplast;s_Uncultured_bacterium_[67571]
4.57E-2	2.98E-4	8.04E-4	[gP]g_Pseudomonas;s_Pseudomonas_sp._m49-6.2_[78148]
4.60E-2	1.80E-4	5.67E-5	[A]g_Uncultured;s_Propionibacterium_sp._b2m2_[85951]
4.63E-2	1.72E-3	4.38E-3	[gP]g_Enterobacter;s_Uncultured_bacterium_[31817]
4.65E-2	1.08E-4	3.50E-4	[gP]g_B38;s_Uncultured_bacterium_[29887]
4.66E-2	3.53E-4	1.17E-3	[A]g_Candidatus_rhodoluna;s_Uncultured_bacterium_[67020]
4.67E-2	1.64E-3	6.82E-4	[gP]g_Haemophilus;s_Uncultured_bacterium_[831]
4.93E-2	3.33E-4	1.20E-3	[bP]g_Burkholderia;s_Burkholderia_cepacia_[85495]

*[A]=Actinobacteria, [aP]=alpha-Proteobacteria, [bP]=beta-Proteobacteria, [gP]=gamma-Proteobacteria, [F]=Firmicutes, [C]=Cyanobacteria.

Table S3. The proportions of representative SILVA 108 *Staphylococcus* sequences for a given site within each non-carrier. Numbers in parentheses indicate the proportion of staphylococcal sequences with respect to all sequences for that given site within the individual. *Staphylococcus* species assignments are based on phylogenetic analysis, comparing staphylococcal sequences with *Staphylococcus* type strain sequences in SILVA 111 LTP.

Individual		C			G			H		
<i>Staphylococcus</i> type strain	Site	AN (6.62E-2)	MM (2.43E-2)	SR (1.10E-2)	AN (2.71E-2)	MM (7.40E-3)	SR (2.16E-2)	AN (1.80E-1)	MM (1.09E-1)	SR (5.27E-2)
Silva 111	Silva 108									
L36472.Staphylococcus.aureus.ATCC12600	34859	8.00E-4	2.50E-4	2.50E-4	3.33E-4	1.00E-4	7.14E-4	3.00E-4	0	1.00E-4
AB009935.1.Staphylococcus.caprae	91763	3.00E-2	9.25E-3	7.50E-4	1.44E-3	6.00E-4	7.86E-4	2.90E-3	2.00E-3	1.10E-3
D83363.1.Staphylococcus.epidermidis	97762	3.04E-2	1.15E-2	9.50E-3	2.44E-2	6.20E-3	1.95E-2	1.74E-1	1.06E-1	4.88E-2
AB009944.1.Staphylococcus.pasteuri	113067	1.00E-4	2.50E-4	0	0	0	1.43E-4	8.00E-4	4.00E-4	1.80E-3
D83366.1.Staphylococcus.gallinarum	18183	8.00E-4	0	0	0	0	0	0	0	0
AB233327.1.Staphylococcus.saprophyticus.subsp..bovis	9739	0	0	0	0	0	0	1.00E-4	0	0
X66100.1.Staphylococcus.haemolyticus	58496	0	0	0	5.56E-5	0	0	0	0	0
AJ421446.1.Staphylococcus.sciuri.subsp.sciuri	74008	3.00E-4	0	0	0	0	0	0	0	0
AB009936.1.Staphylococcus.cohnii	63420	1.10E-3	2.00E-3	0	0	0	7.14E-5	2.00E-4	1.00E-4	3.00E-4
AB009941.1.Staphylococcus.lugdunensis	50471	6.00E-4	0	0	2.22E-4	1.00E-4	1.43E-4	6.00E-4	8.00E-4	3.00E-4
AF004220.1.Staphylococcus.succinus	56488	0	0	0	5.56E-5	1.00E-4	0	0	0	0
D83370.1.Staphylococcus.lentus	87232	0	0	0	0	0	0	1.00E-4	0	0
L37602.1.Staphylococcus.saccharolyticus	97828	1.90E-3	1.00E-3	5.00E-4	5.00E-4	3.00E-4	1.43E-4	2.00E-4	2.00E-4	1.00E-4
D83358.1.Staphylococcus.auricularis	100082	2.00E-4	0	0	0	0	0	0	0	2.00E-4
FJ389206.1.Staphylococcus.devriesei	82693	0	0	0	0	0	7.14E-5	1.00E-4	1.00E-4	0

Individual		L			M			P		
Staphylococcus type strain	Site	AN (1.50E-3)	MM (4.88E-3)	SR (8.75E-4)	AN (8.51E-2)	MM (3.91E-2)	SR (3.88E-2)	AN (1.83E-2)	MM (1.50E-2)	SR (9.63E-3)
Silva 111	Silva 108									
L36472.Staphylococcus.aureus.ATCC12600	34859	1.67E-4	0	0	3.75E-4	0	1.67E-4	3.33E-4	0	0
AB009935.1.Staphylococcus.caprae	91763	0	3.75E-4	0	1.38E-3	1.13E-3	1.00E-3	0	2.50E-4	0
D83363.1.Staphylococcus.epidermidis	97762	1.33E-3	4.25E-3	6.25E-4	7.74E-2	3.60E-2	3.63E-2	1.70E-2	1.39E-2	8.75E-3
AB009944.1.Staphylococcus.pasteuri	113067	0	0	0	0	0	0	0	0	0
D83366.1.Staphylococcus.gallinarum	18183	0	0	0	0	0	0	0	0	0
AB233327.1.Staphylococcus.saprophyticus.subsp..bovis	9739	0	0	0	1.25E-4	0	0	0	0	0
X66100.1.Staphylococcus.haemolyticus	58496	0	0	0	0	0	0	0	0	0
AJ421446.1.Staphylococcus.sciuri.subsp.sciuri	74008	0	0	0	0	0	0	0	0	0
AB009936.1.Staphylococcus.cohnii	63420	0	0	0	0	0	0	0	0	2.50E-4
AB009941.1.Staphylococcus.lugdunensis	50471	0	2.50E-4	2.50E-4	2.13E-3	3.75E-4	0	6.67E-4	6.25E-4	3.75E-4
AF004220.1.Staphylococcus.succinus	56488	0	0	0	0	0	0	1.67E-4	0	1.25E-4
D83370.1.Staphylococcus.lentus	87232	0	0	0	0	0	0	0	0	1.25E-4
L37602.1.Staphylococcus.saccharolyticus	97828	0	0	0	3.50E-3	1.63E-3	1.33E-3	0	2.50E-4	0
D83358.1.Staphylococcus.auricularis	100082	0	0	0	0	0	0	0	0	0
FJ389206.1.Staphylococcus.devriesei	82693	0	0	0	2.50E-4	0	0	1.67E-4	0	0

Table S4. The proportions of representative SILVA 108 *Staphylococcus* sequences for a given site within each carrier. Numbers in parentheses indicate the proportion of staphylococcal sequences with respect to all sequences for that given site within the individual. *Staphylococcus* species assignments are based on phylogenetic analysis, comparing staphylococcal sequences with *Staphylococcus* type strain sequences in SILVA 111 LTP.

Individual:		D			N			Q		
<i>Staphylococcus</i> type strain	Site:	AN (1.62E-1)	MM (2.07E-1)	SR (4.02E-1)	AN (1.86E-1)	MM (1.58E-2)	SR (4.09E-2)	AN (1.24E-1)	MM (5.60E-1)	SR (7.30E-2)
Silva 111	Silva 108									
L36472. <i>Staphylococcus.aureus</i> .ATCC12600	34859	1.46E-1	1.70E-1	3.90E-1	3.50E-3	8.33E-4	1.10E-2	1.92E-2	1.00E-2	1.43E-2
AB009935.1. <i>Staphylococcus.caprae</i>	91763	1.80E-3	3.30E-3	1.00E-4	8.00E-3	2.50E-3	1.24E-2	2.60E-2	6.10E-3	1.04E-2
D83363.1. <i>Staphylococcus.epidermidis</i>	97762	1.00E-2	2.69E-2	9.10E-3	1.67E-1	1.13E-2	1.54E-2	6.76E-2	3.39E-2	4.17E-2
AB009944.1. <i>Staphylococcus.pasteuri</i>	113067	1.00E-4	0	0	0	0	1.25E-4	8.00E-4	2.00E-4	1.30E-3
D83366.1. <i>Staphylococcus.gallinarum</i>	18183	0	0	0	0	1.67E-4	0	0	0	0
AB233327.1. <i>Staphylococcus.saprophyticus</i> .su bsp..bovis	9739	1.00E-4	0	0	0	3.33E-4	0	0	0	0
X66100.1. <i>Staphylococcus.haemolyticus</i>	58496	0	0	0	0	0	1.25E-4	1.00E-4	2.00E-4	1.00E-4
AJ421446.1. <i>Staphylococcus.sciuri</i> .subsp.sciuri	74008	0	0	0	0	0	0	0	0	0
AB009936.1. <i>Staphylococcus.cohnii</i>	63420	3.00E-4	0	3.00E-4	0	0	0	3.00E-4	1.00E-4	3.00E-4
AB009941.1. <i>Staphylococcus.lugdunensis</i>	50471	1.90E-3	3.40E-3	2.00E-3	0	1.67E-4	3.75E-4	1.00E-3	1.50E-3	1.10E-3
AF004220.1. <i>Staphylococcus.succinus</i>	56488	0	0	0	5.00E-4	0	0	0	0	0
D83370.1. <i>Staphylococcus.lentus</i>	87232	0	0	0	0	1.67E-4	0	0	0	0
L37602.1. <i>Staphylococcus.saccharolyticus</i>	97828	1.90E-3	3.10E-3	6.00E-4	7.00E-3	3.33E-4	6.25E-4	5.70E-3	1.70E-3	2.20E-3
D83358.1. <i>Staphylococcus.auricularis</i>	100082	0	3.00E-4	0	0	0	0	3.50E-3	2.30E-3	1.50E-3
FJ389206.1. <i>Staphylococcus.devriesei</i>	82693	0	0	0	0	0	8.75E-4	0	0	1.00E-4

Individual:		R			S			T		
<i>Staphylococcus</i> type strain	Site:	AN (2.65E-1)	MM (1.71E-1)	SR (2.35E-1)	AN (1.09E-1)	MM (9.31E-2)	SR (1.15E-1)	AN (2.35E-1)	MM (1.57E-1)	SR (2.46E-1)
Silva 111	Silva 108									
L36472.Staphylococcus.aureus.ATCC12600	34859	1.21E-1	2.90E-2	1.33E-2	6.25E-4	5.00E-4	0	1.44E-1	7.63E-2	1.73E-1
AB009935.1.Staphylococcus.caprae	91763	4.00E-4	5.00E-4	1.67E-4	1.96E-2	1.20E-2	4.50E-3	5.63E-3	5.50E-3	3.25E-3
D83363.1.Staphylococcus.epidermidis	97762	1.43E-1	1.40E-1	2.22E-1	7.66E-2	7.04E-2	9.90E-2	8.10E-2	7.31E-2	6.76E-2
AB009944.1.Staphylococcus.pasteuri	113067	0	0	0	1.25E-4	1.25E-4	0	0	0	0
D83366.1.Staphylococcus.gallinarum	18183	0	0	0	0	0	0	1.25E-4	1.25E-4	0
AB233327.1.Staphylococcus.saprophyticus.su bsp..bovis	9739	1.00E-4	0	0	1.25E-4	0	0	0	0	0
X66100.1.Staphylococcus.haemolyticus	58496	0	0	0	0	1.25E-4	0	0	3.75E-4	0
AJ421446.1.Staphylococcus.sciuri.subsp.sciuri	74008	0	1.25E-4	0	0	0	0	0	0	0
AB009936.1.Staphylococcus.cohnii	63420	3.00E-4	0	0	0	1.25E-4	0	3.75E-4	0	0
AB009941.1.Staphylococcus.lugdunensis	50471	4.00E-4	6.25E-4	0	1.00E-3	3.75E-4	0	7.50E-4	1.25E-4	3.75E-4
AF004220.1.Staphylococcus.succinus	56488	0	0	0	0	0	0	0	0	0
D83370.1.Staphylococcus.lentus	87232	0	0	0	0	0	0	0	0	0
L37602.1.Staphylococcus.saccharolyticus	97828	1.00E-4	3.75E-4	3.33E-4	9.50E-3	8.75E-3	1.08E-2	3.38E-3	1.38E-3	2.63E-3
D83358.1.Staphylococcus.auricularis	100082	0	0	0	7.50E-4	5.00E-4	2.50E-4	0	0	0
FJ389206.1.Staphylococcus.devriesei	82693	0	0	0	1.25E-4	2.50E-4	5.00E-4	0	0	0

Table S5. OTUs that are significantly enriched in a particular *S. aureus* carriage type (Carrier vs. Non-Carrier) based on ANOVA testing. Relative OTU abundances for persistent carriers (Carrier) were compared with non-persistent (Non-Carrier). P-values were corrected using the false discovery rate (FDR) method. Dark blue highlights enrichment in a particular carriage type and light blue indicates significant lower abundance in the respective other carriage type. The results shown in **Table S5A** derive from data and samples collected at all four time points. The results shown in **Table S5B** derive from data and samples collected at only the first time point.

S5A.

p-value (FDR corrected)	Carrier	Non-Carrier	SILVA 108 OTU [ID]*
1.57E-12	9.79E-2	1.24E-2	[A] g_Corynebacterium; s_Corynebacterium_accolens_atcc_49725 [62359]
1.53E-11	1.23E-2	1.50E-1	[A] g_Corynebacterium; s_Corynebacterium_pseudodiphtheriticum [93808]
2.59E-11	2.00E-2	1.62E-1	[A] g_Corynebacterium; s_Uncultured_bacterium [61264]
1.05E-10	2.95E-3	1.17E-1	[F] g_Dolosigranulum; s_Uncultured_dolosigranulum_sp. [70415]
4.00E-6	1.37E-2	2.37E-3	[F] g_Streptococcus; s_Streptococcus_sp._oral_taxon_070 [96729]
8.32E-5	2.81E-3	5.99E-4	[F] g_Staphylococcus; s_Uncultured_bacterium [97828]
1.88E-4	1.68E-3	2.66E-4	[F] g_Gemella; s_Gemella_sanguinis_m325 [52528]
2.03E-4	1.05E-2	4.54E-5	[gP] g_Raoultella; s_Enterobacter_aerogenes [89546]
2.13E-4	2.07E-1	1.04E-1	[A] g_Propionibacterium; s_Propionibacterium_acnes [92374]
5.76E-4	7.41E-2	1.91E-4	[F] c_Bacilli; g_Staphylococcus; s_Staphylococcus_aureus_st398 [34859]
6.87E-4	7.85E-4	1.15E-4	[F] g_Granulicatella; s_Uncultured_granulicatella_sp. [64052]
1.03E-3	7.53E-4	7.21E-5	[A] g_Corynebacterium; s_Corynebacterium_sp._110960 [58103]
1.57E-3	4.78E-4	7.18E-5	[A] g_Actinomyces; s_Uncultured_bacterium [90234]
1.86E-3	6.29E-2	2.48E-2	[A] g_Tomitella; s_Uncultured_actinobacterium [19852]
2.22E-3	9.11E-4	6.08E-5	[bP] g_Neisseria; s_Uncultured_bacterium [113374]
2.10E-3	5.74E-4	1.10E-5	[F] g_Staphylococcus; s_Uncultured_firmicutes_bacterium [100082]
2.71E-3	2.12E-5	2.15E-4	[A] g_Corynebacterium; s_Corynebacterium_sp. [3878]
5.47E-3	1.80E-3	2.17E-4	[B] g_Prevotella; s_Uncultured_bacterium [85304]
5.53E-3	9.59E-4	5.02E-6	[A] g_Corynebacterium; s_C_glucuronolyticum_atcc_51867 [69247]
5.27E-3	5.37E-4	1.47E-4	[F] g_P5d1-392; s_Bacterium_enrichment_culture_clone_src_dsc20 [30620]
5.20E-3	1.07E-3	3.35E-4	[F] g_Streptococcus; s_Uncultured_bacterium [72538]
5.18E-3	1.21E-3	7.84E-6	[A] g_Corynebacterium; s_Uncultured_bacterium [74770]
6.53E-3	2.80E-3	1.01E-5	[eP] g_Campylobacter; s_Campylobacter_ureolyticus [78595]

S5B.

p-value	Carrier	Non-Carrier	SILVA 108 OTU [ID]*
9.24E-04	1.13E-01	1.67E-02	[A] g_Corynebacterium; s_Corynebacterium_accolens_atcc_49725 [62359]
2.36E-03	4.94E-03	1.13E-01	[A] g_Corynebacterium; s_Corynebacterium_pseudodiphtheriticum [93808]

6.15E-04	1.46E-02	1.14E-01	[A] g_Corynebacterium; s_Uncultured_bacterium [61264]
2.39E-02	6.33E-03	2.17E-03	[F] g_Streptococcus; s_Streptococcus_sp._oral_taxon_070 [96729]
2.81E-02	4.00E-03	1.03E-03	[F] g_Staphylococcus; s_Uncultured_bacterium [97828]
5.31E-02	9.17E-04	3.61E-04	[F] g_Gemella; s_Gemella_sanguinis_m325 [52528]
5.65E-03	1.89E-01	8.23E-02	[A] g_Propionibacterium; s_Propionibacterium_acnes [92374]
3.51E-02	9.68E-02	1.11E-04	[F] c_Bacilli; g_Staphylococcus; s_Staphylococcus_aureus_st398 [34859]
7.99E-02	2.06E-03	1.67E-04	[B] g_Prevotella; s_Uncultured_bacterium [85304]

*[A]=Actinobacteria, [bP]=beta-Proteobacteria, [gP]=gamma-Proteobacteria, [F]=Firmicutes.

Table S6. Intra-individual environments with taxonomic compositional data exhibiting significant C-scores, related to Fig 6. C-scores were calculated using data from a single time point.

OTU-level		
Subject (habitat)	C-score	P-value (Observed>Expected)
D (skin-like)	0.43514	p<0.00001
D (mucosa)	1.64278	p<0.00001
H (mucosa)	2.51998	p<0.00001
Q (mucosa)	2.18889	p<0.00001
T (mucosa)	1.23648	p<0.00001
Genus-level		
Subject (habitat)	C-score	P-value (Observed>Expected)
D (skin-like)	0.27911	p<0.00001
D (mucosa)	0.74234	p<0.00001
G (mucosa)	2.53453	p<0.00001
N (mucosa)	0.88471	p<0.00001
Q (mucosa)	0.87873	P=0.0288
T (mucosa)	0.23478	p<0.00001

Supplemental Experimental Procedures

Co-occurrence Analysis

Patterns for taxon co-occurrence were tested using the program EcoSim (Gotelli and Entsminger, 2011) based upon the Stone and Roberts C-score (Stone and Roberts, 1990) and have previously been used with human microbial datasets (Bik et al., 2010). The number of samples within the dataset in which a particular taxon pair is absent (the checkerboard score) is calculated for a given taxon pair within a matrix. The C-score is then determined as the average checkerboard score of all possible taxon pairs in the matrix and compared to a C-score from randomly generated null matrices of the same size. An observed C-score that is significantly larger than the expected C-score is interpreted as significant segregation and possible competitive exclusion. Calculations were performed at both the OTU level ($n = 2042$) and at the genus level ($n = 187$) where n is the number of distinct taxa.

Co-occurrence analysis was performed using a dataset encompassing a single time point ($T=1$) for all individuals. This limitation was placed to remove temporal effects from convoluting presence/absence data. For co-occurrence results to be informative, the environment must also be assumed to be the same. Previous analysis seemed to indicate that persistent versus non-persistent carriage corresponded to “different environments.” The data was thus further partitioned into subsets designated by *S. aureus* carriage status. The Stone and Roberts C-score was then calculated for these subsets. For both carriers and non-carriers (Table S5), the observed C-score was

significantly greater than the expected and the null-hypothesis of a random distribution of taxon could be rejected. The datasets were further subdivided based on tissue type. C-scores were calculated for the anterior naris samples of carriers separately from the mucosal samples. This process was repeated for the non-carriers and conducted at both the genus and 97% OTU level. At the genus level, the null hypothesis could only be rejected for the mucosal samples of the carriers. At the 97% OTU level, the null hypothesis was rejected for the anterior naris and mucosal samples of carriers, as well as the mucosal samples of non-persistent carriers. The anterior naris samples of the non-persistent carriers comprised the only dataset in which the pattern did not indicate significant segregation.

Staphylococcus phylogenetic reconstruction and taxonomic assignments

Fifteen *Staphylococcus* OTUs were identified in the dataset of twelve human subjects. One representative sequence for each of our *Staphylococcus* OTUs and the respective (most closely related) reference sequence from the SILVA 108 database (total = 30 sequences) were aligned together using SINA (SILVA Incremental Aligner) (Pruesse et al., 2012). Alignments were inspected manually and trimmed to the same length (156 bases). We then calculated sequence identities, and inferred a phylogeny. Maximum likelihood phylogenetic inferences for the resulting alignments were derived using PHYML (Guindon and Gascuel, 2003) with the HKY85 model (Hasegawa et al., 1985) for nucleotide substitutions. Support for the inferred relationship was assessed with 1000 bootstrap replicates. See Fig. S1A for these results. A distance matrix was generated, representing the percent sequence identity for each sequence pair. The

average sequence similarity of our 16S rDNA sequences to the reference OTUs in the SILVA 108 database was 99.6% (SD=0.46).

In addition, the *Staphylococcus* OTUs found in the human nasal cavities were aligned to the 55 *Staphylococcus* reference sequences of the SILVA LTP type strain collection version 111 using SINA, and their percent sequence similarities calculated and displayed in a distance matrix. The *Staphylococcus* type strain that had the highest sequence similarity to our staphylococcal sequence was chosen to assign a species name to our sequences. The average sequence similarity of our 16S rDNA sequences with fifteen respective *Staphylococcus* type strains in the SILVA 111 LTP collection was 99.7% (SD=0.47); 9 of our 15 sequences were 100% identical to their respective *Staphylococcus* type strain sequence, and 4 of our 15 sequences had a 99.4% sequence similarity to their respective type strain and a lower sequence similarity to all other *Staphylococcus* type strains. The distance matrix of sequence similarities is provided as Table S1.

Whereas the V3 region is suitable for distinguishing the fifteen cultivated *Staphylococcus* type strains as well as our staphylococcal sequences (Table S1), the V4 16S rRNA region is not suitable for distinguishing these strains (unpublished results).

Scripts for DPCoA and sparse LDA

```
# for DPCoA  
library(ape)
```

```

library(ade4)

otuTab = read.delim('NewOTUTables_SC/SCtrim5_otutable.txt', row.names = 1)
tree = read.tree('NewOTUTables_SC/SupC_reptree.tre')
dpcoaBase = dpcoa(log(1 + otuTab), tree, scannf = FALSE, nf = 2)

# plotting the communities
plot(dpcoaBase$l2)

# plotting the species
plot(dpcoaBase$l1)


# for sparse LDA -- this is mostly about formatting for specific requirements
of

# the sda function

library(sparseLDA)

speciesData =
read.delim('sparseLDA_input_MYNose_Sil108_species_noJ_noskin_noEukaryota_rare
2000.txt', header = TRUE, row.names = 1)

# the data matrix needs to have variables as columns

speciesData = t(speciesData)

# get the mapping between OTU# and species name

speciesNames =
read.delim('sparseLDA_input_MYNose_Sil108_species_noJ_noskin_noEukaryota_rare
2000.txt', header = TRUE, row.names = 1)

speciesNames = speciesNames[,dim(speciesNames)[2]]

names(speciesNames) = colnames(speciesData)

# normalization object for species data

speciesDataN = normalize(speciesData)

# normalized data matrix for species data

speciesN = speciesDataN$Xc

# carriage status in the form sparse LDA wants it

mappingFile = read.delim('../MYNose_Sil108_trimmed_mapping.txt', row.names =
1)

```

```

carriageStatus = matrix(as.numeric(mappingFile[rownames(speciesData), 7] ==
'Carrier'), ncol = 1)

carriageStatus = cbind(carriageStatus, 1 - carriageStatus)

colnames(carriageStatus) = c('Carrier', 'Non-Carrier')

# sparse LDA with 10 OTUs

sda(speciesN, carriageStatus, stop = -10)

```

Bacterial cultivation and interaction assays

Corynebacterium accolens ATCC 49725, *Corynebacterium pseudodiphtheriticum* DSM 44287, and *Staphylococcus aureus* COL were used for bacterial agar plate interaction assays. *Corynebacterium* strains were streaked out from glycerol stock cultures on Brain Heart Infusion (BHI) Agar (Becton Dickinson) with 1% Tween 80 (Fisher Scientific) (Goodfellow, 2012), and *Staphylococcus aureus* was streaked out on BHI agar. All strains were incubated at 35 degree Celsius for 24 hours. For bacterial interaction assays BHI in double distilled water with 1.5% agar (Fischer Scientific) and 0.5% Tween 80 were mixed, the suspension shortly boiled, allowed to cool to 55 degree Celsius, and the pH was adjusted to either 5.5 or 6.5 with glacial acetic acid (Fisher Chemicals). The medium was autoclaved at 120 degree Celsius for 20 min, and cooled to 55 degree Celsius. Bacterial cells were carefully harvested from agar plates with an inoculation loop and 0.04 g cells re-suspended in 0.2 ml sterile 0.9% sodium chloride (Mallinckrodt Chemicals) solution. Eight microliter of the cell suspension were added to 15 ml of prepared liquid BHI agar, mixed and poured into a sterile Petri dish. The agar was allowed to cool for 30 min in a sterile laminar flow cabinet. Subsequently, 25 microliter of a bacterial cell suspension was placed in the center of the plate on top of the agar and allowed to dry for 40 min in a sterile laminar flow cabinet. For growth interference of

corynebacteria by *S. aureus* BHI-Tween pH 5.5 was used, and plates were incubated for 24 h at 35 degree Celsius. For growth interference of *S. aureus* by corynebacteria BHI-Tween pH 6.5 was used, and plates were incubated for 16 h at 35 degree Celsius and subsequently for 24 h at room temperature. Agar plates were inspected and the distance between the border of the spotted colony and the periphery of the inhibition- or growth promotion zone was measured.

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